

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.
 M nucleic - nucleic search, using sw model
 run on: July 11, 2006, 07:21:26 ; Search time 107.065 Seconds
 (without alignments)
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 title: US-09-973-994-131
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 Gapop 10_0 , Gapext 1.0
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 total number of hits satisfying chosen parameters: 2807332
 Sequence 774, App
 Sequence 3, Appli
 Sequence 3, Appli
 Sequence 17486, A
 Sequence 11750, A
 Sequence 16934, A
 Sequence 12033, A
 Sequence 113225, A
 Sequence 12287, A
 Sequence 14864, A
 Sequence 14179, A
 Sequence 30681, A
 Sequence 14410, A
 Sequence 3, Appli
 Sequence 3, Appli
 Sequence 12739, A
 Sequence 13946, A
 Sequence 11755, A
 Sequence 12936, A
 Sequence 1, Appli
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 Sequence 2607, Ap

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries						
Issued Patents_NA: *						
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SUMMARIES						
* Query No. Score Match Length DB ID Description						
1 37.6 14.4 144362 3 US-09-949-016-16066 Sequence 16066, A						
2 36.8 14.1 357 3 US-09-640-211A-1581 Sequence 1581, AP						
3 35.8 13.7 264206 3 US-09-949-016-12731 Sequence 12731, A						
4 35.8 13.7 264304 3 US-09-949-016-13249 Sequence 13249, A						
5 35.6 13.6 117391 3 US-09-949-016-13945 Sequence 13945, A						
6 34.8 13.3 139049 3 US-09-949-016-17030 Sequence 17030, A						
7 34.8 13.3 193555 3 US-09-949-016-15553 Sequence 15553, A						
8 34.8 13.3 193555 3 US-09-949-016-15554 Sequence 15554, A						
9 34.8 13.3 193555 3 US-09-949-016-15555 Sequence 15555, A						
10 34.6 13.3 200663 3 US-09-949-016-12569 Sequence 12569, A						
11 34.6 13.3 203093 3 US-09-949-016-14445 Sequence 14445, A						
12 33.6 12.9 601 3 US-09-949-016-53593 Sequence 53593, A						
13 33.6 12.9 57392 3 US-09-949-016-12070 Sequence 12070, A						
14 33.6 12.9 57402 3 US-09-949-016-13293 Sequence 13293, A						
15 33.4 12.8 786 3 US-09-949-016-14445 Sequence 905, APP						
16 33.2 12.7 43360 3 US-09-453-702B-206 Sequence 206, APP						
17 33.2 12.7 45325 3 US-09-453-702B-261 Sequence 261, APP						
18 33.2 12.7 45325 3 US-10-114-170-261 Sequence 261, APP						
19 33.2 12.7 156324 3 US-09-949-016-13749 Sequence 13749, A						
20 33.2 12.7 156324 3 US-09-949-016-13749 Sequence 13749, A						
21 33.2 12.6 237863 3 US-09-949-016-13404 Sequence 13404, A						
22 32.8 12.6 150 5 US-09-974-300-7683 Sequence 7683, APP						
23 32.8 12.6 56374 3 US-09-949-002-645 Sequence 645, APP						

RESULT 2

US-09-640-211A-1581
 ; Sequence 1581, Application US/09640211A
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, Marion
 ; APPLICANT: Shenk, Michael A.
 ; APPLICANT: McGrath, Annette
 ; APPLICANT: Glenn, Matthew
 TITLE OF INVENTION: Compositions and Methods for the
 TITLE OF INVENTION: Modification of Gene Transcription
 FILE REFERENCE: 11000.1021CU
 CURRENT APPLICATION NUMBER: US/09/640, 211A
 CURRENT FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 2368
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1581
 LENGTH: 357
 TYPE: DNA
 ORGANISM: Pinus radiata
 US-09-640-211A-1581

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 Best Local Similarity 52.6%; Pred. No. 0.31;
 Matches 80; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 46 AGTTTTCCGATTCCGTGTGAGGGACGGAAACGAGATAAGTTGCTAAAGTTGCTCGCT 105
 Db 85 AGTTCACTCTGGTTCACTTGGACTATACAACAGAACAAATTTGAAATGCTCTAGCT 144

Qy 106 GATTTGGGGCACGGAAACGGAGATAAGTTGCTGATTTTGCTGAA 165
 Db 145 GATTTTGATAAAGACACCCCAAGATAATGGGAGAAAGTGGCAGGCCAGCTGGAAAPA 204

Qy 166 TATTTCTCTCACTATAAAGCATTTCAGA 197
 Db 205 ACTGCTACGGATGTAGAAAGCCATTATGAGA 236

RESULT 3

US-09-949-016-12731/C
 ; Sequence 12731, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231, 498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 12731
 LENGTH: 264206
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-12731

Query Match 13.7%; Score 35.8; DB 3; Length 264206;
 Best Local Similarity 52.3%; Pred. No. 4.3%;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 45 AAGTTTTCCGATTCCGTGTGAGGGACGGAAACGAGATAAGTTGCTAAAGTTGCTCGC 104
 Db 14095 AAATATTCAAAATCATTGGACTTCAGTAATCCAAAGAGAAATTTGGAAATTTCTCTA 14036

Qy 105 TGATTTGGGGCACGGAAACGAGATAAGTTGCTGATTTTGCTGCTGATTTGCTGA 164
 Db 14035 AAATTAATCCAGAACACAAAGGTTCAGTTGGAAATAATGGAAAGCATTTGCTTTAA 13976

Qy 165 ATATTTCTCTCACTATAAAGCATTTCAGA 195
 Db 13975 AAATCTAAACATTTTAAAGACAAATTTCA 13945

RESULT 4

US-09-949-016-13249/C
 ; Sequence 13249, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231, 498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13945
 LENGTH: 117391
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-13249

Query Match 13.7%; Score 35.8; DB 3; Length 264304;
 Best Local Similarity 52.3%; Pred. No. 4.3%;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 45 AGTTTTCCGATTCCGTGTGAGGGACGGAAACGAGATAAGTTGCTAAAGTTGCTCGC 104
 Db 14095 AAATATTCAAAATCATTGGACTTCAGTAATCCAAAGAGAAATTTGGAAATTTCTCTA 14036

Qy 105 TGATTTGGGGCACGGAAACGAGATAAGTTGCTGATTTTGCTGCTGATTTGCTGA 164
 Db 14035 AAATTAATCCAGAACACAAAGGTTCAGTTGGAAATAATGGAAAGCATTTGCTTTAA 13976

Qy 165 ATATTTCTCTCACTATAAAGCATTTCAGA 195
 Db 13975 AAATCTAAACATTTTAAAGACAAATTTCA 13945

RESULT 5

US-09-949-016-13945/C
 ; Sequence 13945, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231, 498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13945
 LENGTH: 117391
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-13945

Query Match 13.7%; Score 35.8; DB 3; Length 264206;
 Best Local Similarity 52.3%; Pred. No. 4.3%;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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 Db 14095 AAATATTCAAAATCAATGGACCTCAAGTAATCCAAAGAGAAATTTGGAAACATTTCTCTA 14036

Qy 105 TGATTTGGGGCACGGAAACGAGATAAGTTGCTGATTTTGCTGCTGATTTGCTGA 164

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OM nucleic - nucleic search, using sw model
 Run on: July 11, 2006, 07:46:06 ; Search time 53.7623 Seconds
 (without alignments)
 6311.756 Million cell updates/sec

Title: US-09-973-994-131
 Perfect score: 261
 Sequence: 1 aggtgaccgtacaggatata.....gggtttttccacggtcacct 261
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 844069 seqs, 650066433 residues
 Total number of hits satisfying chosen parameters: 1688138

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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 Listing First 45 summaries

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 * Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	36.4	13.9	962	8	US-11-266-748A-97714	Sequence 97714, A	Sequence 150525, Sequence 361361, Sequence 444740, Sequence 260726, Sequence 321243, Sequence 192101, Sequence 226177, Sequence 55772, A
C	2	36.4	13.9	962	8	US-11-266-748A-150525	Sequence 166299, Sequence 172138, Sequence 19927, A
C	3	36.4	13.9	1421	8	US-11-266-748A-361361	Sequence 118940, Sequence 161104, Sequence 224558, Sequence 293755,
C	4	36.4	13.9	1421	8	US-11-266-748A-444740	Sequence 28652, A
	5	36.4	13.9	1888	8	US-11-266-748A-260726	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	6	36.4	13.9	1888	8	US-11-266-748A-321243	Sequence 118940, Sequence 161104, Sequence 224558, Sequence 293755,
C	7	35.8	13.7	988	8	US-11-266-748A-192101	Sequence 28652, A
	8	35.8	13.7	988	8	US-11-266-748A-226177	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	9	35.4	13.6	686	8	US-11-266-748A-55772	Sequence 118940, Sequence 161104, Sequence 224558, Sequence 293755,
C	10	34.4	13.2	706	8	US-11-266-748A-166299	Sequence 28652, A
C	11	34	13.0	489	8	US-11-266-748A-172138	Sequence 118940, Sequence 161104, Sequence 224558, Sequence 293755,
C	12	34	13.0	888	8	US-11-266-748A-19927	Sequence 28652, A
C	13	33.8	13.0	2079	8	US-11-266-748A-180693	Sequence 28652, A
C	14	33.6	12.9	3350	8	US-11-266-748A-28652	Sequence 28652, A
C	15	32.6	12.5	1000	8	US-11-266-748A-118940	Sequence 118940, Sequence 161104, Sequence 224558, Sequence 293755,
C	16	32.6	12.5	1000	8	US-11-266-748A-161104	Sequence 28652, A
C	17	32.6	12.5	1000	8	US-11-266-748A-224558	Sequence 28652, A
C	18	32.6	12.5	1000	8	US-11-266-748A-293755	Sequence 28652, A
C	19	32.6	12.5	1000	8	US-11-266-748A-345184	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	20	32.6	12.5	1000	8	US-11-266-748A-396868	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	21	32.6	12.5	1000	8	US-11-266-748A-405877	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	22	32.6	12.5	1000	8	US-11-266-748A-467914	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	23	32.6	12.5	1000	8	US-11-266-748A-476923	Sequence 345184, Sequence 396868, Sequence 405877, Sequence 467914,
C	24	32.6	12.5	2199	6	US-10-471-571A-421	Sequence 421, App

25 32.6 12.5 10884 8 US-11-266-748A-29503 Sequence 29503, A
 26 32.6 12.5 10935 8 US-11-266-748A-56647 Sequence 56647, A
 27 32.2 12.3 795 8 US-11-266-748A-87473 Sequence 87473, A
 C 28 32.2 12.3 795 8 US-11-266-748A-140284 Sequence 140284, A
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 Sequence 2370, Ap
 Sequence 31160, A
 Sequence 31694, A
 Sequence 23, App
 Sequence 29039, A
 Sequence 253, App
 Sequence 26679, A
 Sequence 826, App
 Sequence 420002, App
 Sequence 11128, A
 Sequence 369370, A
 Sequence 452749, A
 Sequence 242695, A

ALIGNMENTS

RESULT 1
 US-11-266-748A-97714
 ; Sequence 97714, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; METHODS OF USING THE SAME
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266,748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 97714
 ; LENGTH: 962
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (231)
 ; OTHER INFORMATION: n is a, c, g, or t
 ; US-11-266-748A-97714
 ; Query Match 13.9%; Score 36.4; DB 8; Length 962;
 ; Best Local Similarity 53.5%; Pred. No. 0.77;
 ; Mismatches 66; Indels 0; Gaps 0;
 ; Matches 76; Conservative 0;
 ; QY 75 AAACGAGATAAAGTTGTAAGTTGCTCGTGTAGGGACGGAAAAACGAGATAAGTT 134

Db 799 ACACAAGCCTCATGGTAAATTTCACACTGAGTTACCAACAGGGCTTAACATCTGTC 858

Qy 135 GTAAAATTGGCTGATTGGCTGAAATTCTCACTATAAAAGCATTTC 194

Db 859 TTGCTCTTACACGAAACATGAGTGAATCCCTGCTCACTAGTCCAAGCATTCC 918

Qy 195 AGAAATAGAAGGGCTTCGA 216

Db 919 AGCAAAAGATCCAGCCATCAA 940

RESULT 2
US-11-266-748A-150525/C

; Sequence 150525, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479-2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482-6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483-4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507-0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485-9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484-2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 041054276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO: 361361

; LENGTH: 1421

; TYPE: DNA

; ORGANISM: Homo Sapiens

; US-11-266-748A-361361

Query Match 13.9%; Score 36.4; DB 8; Length 1421;

Best Local Similarity 53.5%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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Db 164 ACACAAAGCCTCATGGTAAATTTCACACTGAGTTACCCACAGGGCTTAACATCTGTC 105

Qy 135 GTAAATTGCTCGTGTGATTTTGCTGAATATTCTCACTATAAAAGCATTTC 194

Db 104 TTGCTCTCTTACACGAAACATGAGTGAATCCCTTGCTCACTAGTCCARGCATTCTCC 45

Qy 195 AGAAATAAGAAGGGCTTCGA 216

Db 44 AGCAAAAGATCCAGCCATCAA 23

RESULT 4

US-11-266-748A-444740

; Sequence 444740, Application US/1126,6748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479-2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482-6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483-4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507-0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485-9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 041054293

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507-0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485-9

; PRIOR FILING DATE: 2004-11-03

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; PRIOR APPLICATION NUMBER: EP 04105507-0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507-0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507-0

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; PRIOR APPLICATION NUMBER: EP 04105507-0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:46:32 ; Search time 779.324 Seconds
 (without alignments)
 4115.199 Million cell updates/sec

Title: US-09-973-994-131
 Perfect score: 261
 Sequence: 1 aggtgaccgtacaggattta.....99gtttttcacggtaacct 261

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_Main:
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 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:
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 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:
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 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:
 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:
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 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	261	100.0	261	10	US-10-651-991-131		Sequence 131, App
2	37.4	14.3	40324	8	US-10-433-793-180		Sequence 180, App
3	37	14.2	346	4	US-09-925-065A-125478		Sequence 125478,
4	37	14.2	346	4	US-09-925-065A-125480		Sequence 125480,
5	37	14.2	346	4	US-09-925-065A-125481		Sequence 125481,
6	37	14.2	346	5	US-09-925-065A-125478		Sequence 125478,
7	37	14.2	346	5	US-09-925-065A-125480		Sequence 125480,
8	37	14.2	346	5	US-09-925-065A-125481		Sequence 125481,
9	37	14.2	558	4	US-09-925-065A-439656		Sequence 439656,
10	37	14.2	558	5	US-09-925-065A-439656		Sequence 439656,
11	36.8	14.1	357	9	US-10-856-499-1581		Sequence 1581, App
12	36.8	14.1	5276	7	US-10-311-455-800		Sequence 800, App
13	36.8	14.1	5276	8	US-10-221-714A-102		Sequence 102, App
14	36.8	14.1	40862	7	US-10-311-455-2046		Sequence 2046, App
15	36.6	14.0	346	4	US-09-925-065A-125479		Sequence 125479,
16	36.6	14.0	346	5	US-09-925-065A-125479		Sequence 125479,
17	36	13.8	37515	8	US-10-433-793-27		Sequence 27, Appl

C 18 35.8 13.7 608 4 US-09-925-065A-787534
 C 19 35.8 13.7 608 5 US-09-925-065A-787534
 C 20 35.8 13.7 611 4 US-09-925-065A-73437
 C 21 35.8 13.7 611 5 US-09-925-065A-73437
 C 22 35.8 13.7 611 12 US-10-301-480-174676
 C 23 35.8 13.7 611 12 US-10-301-480-788085
 C 24 35.8 13.7 654 4 US-09-925-065A-778843
 C 25 35.8 13.7 654 4 US-09-925-065A-778844
 C 26 35.8 13.7 654 5 US-09-925-065A-778843
 C 27 35.8 13.7 654 5 US-09-925-065A-778844
 C 28 35.8 13.7 680 4 US-09-925-065A-785063
 C 29 35.8 13.7 680 4 US-09-925-065A-785064
 C 30 35.8 13.7 680 4 US-09-925-065A-785065
 C 31 35.8 13.7 680 5 US-09-925-065A-785063
 C 32 35.8 13.7 680 5 US-09-925-065A-785064
 C 33 35.8 13.7 680 5 US-09-925-065A-785065
 C 34 35.8 13.7 823 6 US-10-027-632-172361
 C 35 35.8 13.7 823 7 US-10-027-632-172361
 C 36 35.8 13.7 2325 6 US-10-027-632-103528
 C 37 35.8 13.7 2325 6 US-10-027-632-103529
 C 38 35.8 13.7 2325 7 US-10-027-632-103528
 C 39 35.8 13.7 2325 7 US-10-027-632-103529
 C 40 35.8 13.7 561515 8 US-10-741-601-5682
 C 41 35.8 13.7 561515 9 US-10-741-600-17730
 C 42 35.8 13.7 3673778 7 US-10-312-841-2
 C 43 35.4 13.6 969 12 US-10-301-480-570600
 C 44 35.4 13.6 969 12 US-10-301-480-1184009
 C 45 35.4 13.6 987 12 US-10-301-480-603635
 Sequence 603635,

ALIGNMENTS

RESULT 1
 US-10-651-991-131
 ; Sequence 131, Application US/10651991
 ; Publication No. US20050125161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CAIRNEY, JOHN
 ; APPLICANT: XU, NANFIE
 ; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED CONIFER CDNAS, AND THEIR USE
 ; TITLE OF INVENTION: IN IMPROVING SOMATIC EMBRYOGENESIS
 ; FILE REFERENCE: 7648.0023-00
 ; CURRENT APPLICATION NUMBER: US/10/651_991
 ; CURRENT FILING DATE: 2003-09-02
 ; PRIOR APPLICATION NUMBER: 60/239, 250
 ; PRIOR FILING DATE: 2000-10-11
 ; NUMBER OF SEQ ID NOS: 339
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 131
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Pinus taeda
 ; US-10-651-991-131
 ; Query Match 100.0%; Score 261; DB 10; Length 261;
 ; Best Local Similarity 100.0%; Pred. No. 1.3e-63;
 ; Mismatches 0; Indels 0; Gaps 0;

1 AGGTGACCGTACAGGATTATTGATTTGTTGCAAGTGTCTCGATTTCG 60
 1 AGGTGACCGTACAGGATTATTGATTTGTTGCAAGTGTCTCGATTTCG 60
 1 CTGTGAGGCCAGGAAACGAGATAGTTGCTGATTGTTGCTGAATATTCTCACTAT 120
 1 CTGTGAGGCCAGGAAACGAGATAGTTGCTGATTGTTGCTGAATATTCTCACTAT 120
 1 AACAGGAGATAAGTTGTTAAATTTGCTGATTTGCTGAATATTCTCACTAT 180
 1 AACAGGAGATAAGTTGTTAAATTTGCTGATTTGCTGAATATTCTCACTAT 180

Qy 181 AAAAGCATTTCAGAAATAAGAAGGACTGGTTTCGAACCTCCAAAGAGTTGTTAG 240
 Db 181 AAAAGCATTTCAGAAATAAGAAGGACTGGTTTCGAACCTCCAAAGAGTTGTTAG 240

Qy 241 GGGTTTCCACGGTCACCT 261
 Db 241 GGGTTTCCACGGTCACCT 261

RESULT 2
 US-10-433-793-180
 ; Sequence 180, Application US/1043334A1
 ; Publication No. US20040142334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Epigenomics AG
 ; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/433,793
 ; CURRENT FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 212
 ; SEQ ID NO 180
 ; LENGTH: 40324
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-433-793-180

Query Match 14.3%; Score 37.4; DB 8; Length 40324;
 Best Local Similarity 52.2%; Pred. No. 31;
 Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
 Qy 25 TGTTCTATTTGGTTGCAAGTTTCGATTCCGATTGGCACGGAAACGAGATA 84
 Db 26359 TGTTTAGTTTAATTTTAATTGGTTGTGAAAGATAATTGGGGAGAGTT 26418
 Qy 85 AGTTGTAAAAGGTTGCTCGCTGATTGGAGGAAACGAGATAAGTTGTTAATT 144
 Db 26419 TTTTAAGAAGTTGTTAGATAATAGTTGATGTATAATTAGTT 26478
 Qy 145 GCTCGCTGATTGGCTGAATATTCTCACTATAA 183
 Db 26479 AATTAAAGATTGAGAATTGAGTTGGTGTATATA 26517

RESULT 3
 US-09-925-065A-125478

; Sequence 125478, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 125480
 LENGTH: 346
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-925-065A-125480

Query Match 14.2%; Score 37; DB 4; Length 346;
 Best Local Similarity 52.2%; Pred. No. 5;
 Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
 Qy 84 AGTTGTAAGTTGCTGAATTGGCACGGAAACGAGATAAGTTGTTAAATT 143
 Db 178 AACTGAAAGACACTAATCTGCTGAGCCACAAATCAGATTATCTGTTACCT 237
 Qy 144 TGCTCGCTGATTGGCTGAATTTCTCACTATAAAAGCATTTCCAGAAATAAG 203
 Db 238 GCGTGATTCTTCTGAACTGGTTCCAGAGTTGTAG 240
 Qy 204 AGGGACTTTCGAACTGGTTCCAGAGTTGTAG 240
 Db 298 AAGTTTAACTCTAAGGTAGTGTCAAGTCTCTTGG 334

RESULT 4
 US-09-925-065A-125480
 ; Sequence 125480, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 125480
 LENGTH: 346
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-925-065A-125480

Query Match 14.2%; Score 37; DB 4; Length 346;
 Best Local Similarity 52.2%; Pred. No. 5;
 Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
 Qy 84 AGTTGTAAGTTGCTGAATTGGCACGGAAACGAGATAAGTTGTTAAATT 143
 Db 178 AACTGAAAGACACTAATCTGCTGAGCCACAAATCAGATTATCTGTTACCT 237
 Qy 144 TGCTCGCTGATTGGCTGAATTTCTCACTATAAAAGCATTTCCAGAAATAAG 203
 Db 238 GCGTGATTCTTCTGAACTGGTTCCAGAGTTGTAG 240
 Qy 204 AGGGACTTTCGAACTGGTTCCAGAGTTGTAG 240
 Db 298 AAGTTTAACTCTAAGGTAGTGTCAAGTCTCTTGG 334

RESULT 5
 US-09-925-065A-125481
 ; Sequence 125481, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135

GenCore version 5.1.9
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DM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:01:45 ; Search time 333.602 Seconds
(without alignments)
5454.872 Million cell updates/sec

Title: US-09-973-994-131

Perfect score: 261

Sequence: 1 aggtaccgtacagcattta.....gggttttccacgggtcacct 261

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

RESULT 1
AEA49636
ID AEA49636 standard; cDNA; 261 BP.
XX
AEA49636;
XX
AC
XX
DT 11-AUG-2005 (First entry)
XX
DE Loblolly pine cDNA clone, LPZ-061, SEQ ID 131.
XX
DE Plant; embryogenesis; plant breeding; paper; wood; ss.
XX

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	
1	261	100.0	261	14	AEA49636	Aea49636 Loblolly	
2	37.4	14.3	40324	6	ABQ67150	Abq67150 Human ang	
3	36.8	14.1	357	3	AAC56859	Aac56859 Pinus rad	
4	36.8	14.1	1943	14	ADW16980	Adw16980 Pinus rad	
5	36.8	14.1	5276	4	AAS46380	Aas46380 Tumour su	
6	36.8	14.1	5276	6	ABL32827	Ab132827 Human imm	
7	36.8	14.1	40862	6	ABL34073	Ab134073 Human imm	
8	36.4	13.9	1084	3	AAC59973	Aac59973 Human sec	
9	36	13.8	37515	6	ABQ66997	Abq66997 Human ang	
C	10	35.4	13.6	2000	11	ACL37108	Ac137108 Rice stre
C	11	35.4	13.6	6113	6	ABL32803	Ab132803 Human imm
C	12	35	13.4	1726	11	ADO77946	Ado77946 Brassica
C	13	35	13.4	73334	6	ABL34124	Ab134124 Human imm
C	14	35	13.4	73334	6	ABL92318	Ab192318 Chemical
C	15	34.8	13.3	5542	6	ABL34021	Ab134021 Human imm
C	16	34.8	13.3	11209	6	ABN80136	Abn80136 Human che
C	17	34.6	13.3	2441	14	ADW10461	Adw10461 Colon pro

The present invention relates to a relational database of cDNA molecules comprising multiple nucleotide sequences (AE49506-AEA49832). The database is useful for staging plant embryos, selecting advantageous plant clones, determining embryo fitness, and selecting advantageous plant clones for embryo development. The invention also relates to a method for determining the fitness of plant embryos.

CC For use in breeding trees with superior characteristics for use in
CC production of paper and other wood products.

XX Sequence 261 BP; 69 A; 43 C; 60 G; 89 T; 0 U; 0 Other;

SQ Score 100.0%; Score 261; DB 14; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1e-63;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 AGGTGACCGTACAGCATTATTGATGTTCTTATTGTTGCAAGTTTCGGATTG 60
1 AGGTGACCGTACAGCATTATTGATGTTCTTATTGTTGCAAGTTTCGGATTG 60

Qy 61 CTGTGAGGCCAGGAAACAGGATAAAGTTGTTAAAGTTGCTGATTGGAGGACGG 120
61 CTGTGAGGCCAGGAAACAGGATAAAGTTGTTAAAGTTGCTGATTGGAGGACGG 120

Db 121 AAACGAGATAAAGTTGTAAAATTGCTCGTGAATATTTCCTCTCACTAT 180
121 AAACGAGATAAAGTTGTAAAATTGCTCGTGAATATTTCCTCTCACTAT 180

Qy 181 AAAAAGGATTTCCAGAAATANGAAGGGACTTGGAACTGGTTTCAAGAGTTG 240
181 AAAAAGGATTTCCAGAAATANGAAGGGACTTGGAACTGGTTTCAAGAGTTG 240

Db 241 GGGTTTTTCCACGGTCACCT 261
241 GGGTTTTTCCACGGTCACCT 261

Qy RESULT 2
ABQ67150
ID ABQ67150 standard; DNA; 40324 BP.
XX AC ABQ67150;
XX DT 28-AUG-2002 (first entry)

DE Human angiogenesis associated polynucleotide SEQ ID NO 180.
XX Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
KW inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;
KW macular degeneration; inflammatory bowel disease; Crohn's disease;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiarteriosclerotic; ds.
XX Homo sapiens.
XX OS WO200246454-A2.
XX PN 09-MAR-2000; 2000WO-US006112.

XX PD 13-JUN-2002.
XX PR 11-MAR-1999; 99US-00266513.
PP 06-DEC-2001; 2001WO-EP014320.
XX PR 18-AUG-1999; 99US-0149485P.

XX (EPIG-) EPIGENOMICS AG.
XX PI Wood M, McGrath A, Shenk MA, Glenn M;
XX PI DR WPI; 2000-579369/54.

XX DR WPI; 2000-579369/54.
XX PS Claim 1; SEQ ID NO 180; 41pp + Sequence Listing; German.

XX The invention relates to a nucleic acid (I) comprising a segment of 18
CC bases of chemically pretreated DNA of angiogenesis-associated genes (II)
CC having sequences (ABQ66971-ABQ67178) or their complements. (I), also
CC related oligomers, are used to evaluate the methylation status and/or
CC single-nucleotide polymorphisms, in angiogenesis-related genes, for

CC diagnosis and treatment of eye diseases; proliferative retinopathy,
CC neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
CC diabetic retinopathy, macular degeneration caused by neovascularisation,
CC psoriasis, arteriosclerosis, inflammatory bowel disease, ulcers and
CC Crohn's disease. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 40324 BP; 12266 A; 436 C; 7652 G; 19970 T; 0 U; 0 Other;
XX SQ Query Match 14.3%; Score 37.4%; DB 6; Length 40324;
XX Best Local Similarity 52.2%; Pred. No. 4.7;
XX Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
XX Qy 25 TGTCTATTGTTGCTGTTGCAAGTTTCCGATTGCTGAGGCCAGGATA 84
DB 26359 TGTCTAGTTAAATTTTAAATTGTTGAAAGATAATTGAGGGAGGATT 26418
Qy 85 AGTTGTAAGAAAGTTGCTGATTGAGGACGGAAACCGAGATAAGTTGTA 144
DB 26419 TTGTTAAGAAGTTGTAATAGTTAGATGTATAATTAGTT 26478
Qy 145 GCTCGGTGATTGCTGAATATTCTCTCACTATAA 183
DB 26479 ATTTAAGAAGTTTATTGAGAATAGTTGTTGTTGTT 26517

XX RESULT 3
XX AAC56859
XX ID AAC56859 standard; DNA; 357 BP.
XX AC AAC56859;
XX DT 25-JAN-2001 (first entry)
XX DE Pinus radiata transcription factor DNA sequence #305.
XX KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; EREBES; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB; BS.
XX OS Pinus radiata.
XX PN WO200053724-A2.
XX PD 14-SEP-2000.
XX PF 09-MAR-2000; 2000WO-US006112.

XX PR 11-MAR-1999; 99US-00266513.
PP 18-AUG-1999; 99US-0149485P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX PI Wood M, McGrath A, Shenk MA, Glenn M;
XX DR WPI; 2000-579369/54.

XX PS New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide.
XX Claim 1; Page 531; 747pp; English.

XX The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:10:56 ; Search time 2616.43 Seconds
 (without alignments)
 5578.184 Million cell updates/sec

Title: US-09-973-994-131
 Perfect score: 261
 Sequence: 1 aggtgaccgtacagcatta.....999gtttttccacggtcaccc 261

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : EST:

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2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
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10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
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C 2	89.8	34.4	674	9	DR053876		DR053876 RTCA1_13
C 3	82.4	31.6	817	9	DR120385		DR120385 RTMG1_29
C 4	76	29.1	643	13	CZ895986		CZ895986 226_2_123
C 5	42.2	16.2	1257	7	BE894011		BE894011 601437812
C 6	41.8	16.0	495	8	CO456808		CO456808 MZCCS1500
C 7	40.2	15.4	1101	14	CNS000D1		AL065414 Drosophil
C 8	40.2	15.4	1356	10	DV779559		DV779559 Hw_Fat_57
C 9	40	15.3	783	14	BX197330		BX197330 Danio rer
C 10	39.2	15.0	607	12	CE516027		CE516027 tigr-gss-
C 11	38.8	14.9	694	14	BX158594		BX158594 Danio rer
C 12	38.8	14.9	941	3	BUI53366		BUI53366 AGENCOURT
C 13	38.6	14.8	386	8	CN252666		CN252666 EST018601
C 14	38.6	14.8	663	14	DE073250		DE073250 Oryzias1
C 15	38.6	14.8	1101	14	CNS00EQL		AL069526 Drosophil
C 16	38.6	14.8	1101	14	CNS00ZB7		AL097453 Drosophil
C 17	38.4	14.7	489	4	BX553089		BX553089
C 18	38.4	14.7	856	8	CV595856		CV595856 L_AJ-aaa0
C 19	38.2	14.6	537	12	CE105632		CE105632 tigr-gss-

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 Best Local Similarity 88.9% ; Pred. No. 3e-13 ;
 Matches 120 ; Conservative 0 ; Mismatches 13 ; Indels 2 ; Gaps 2 ;
 /clone_lib="Pine methylation unfiltered library (LibID: 131)"

Qy 127 GATAAGTTGTTAAAATTGCTGAATTTCTCACTATAAAAAG 186

C 20	38.2	14.6	677	11	BZ278020		BZ278020 CH230-356
C 21	38.2	14.6	792	11	BZ455713		BZ455713 BONSH83TF
C 22	37.8	14.5	603	10	DR783465		DR783465 Le_1v0_17
C 23	37.8	14.5	610	10	DR714239		DR714239 Le_1v0_13
C 24	37.8	14.5	620	8	CO049664		CO049664 Le_mx0_03
C 25	37.8	14.5	830	11	AQ750770		AQ750770 HS_5576_B
C 26	37.8	14.5	1505	1	AM102256		AM102256 BP677423
C 27	37.6	14.4	691	3	BP677423		BP677423 Hw_1oin_3
C 28	37.6	14.4	1322	10	DV795774		DV795774 RDEV151_H
C 29	37.4	14.3	620	9	CX506668		CX506668 JGI_XZG51
C 30	37.4	14.3	866	14	DU738879		DU738879 APK14906
C 31	37.4	14.3	908	14	CNS01678		AL106382 Drosophil
C 32	37.2	14.3	299	14	DE245139		DE245139 Trifolium
C 33	37.2	14.3	531	7	AW991228		AW991228 RDEV151_H
C 34	37.2	14.3	650	12	CC847241		CC847241 NDL_109D1
C 35	37.2	14.3	650	12	CC853143		CC853143 NDL_109C1
C 36	37	14.2	448	2	BI275009		BI275009 UI-R-CX0-
C 37	37	14.2	663	2	BI284287		BI284287 UI-R-CX08
C 38	37	14.2	682	14	BX195327		BX195327 Danio rer
C 39	37	14.2	940	13	DU045365		DU045365 153078
C 40	36.8	14.1	788	14	DU591489		DU591489 OO_Ba008
C 41	36.8	14.1	845	14	DU865836		DU865836 82515 Tom
C 42	36.8	14.1	910	14	DU875609		DU875609 147915
C 43	36.8	14.1	963	13	DU082579		DU082579 271367
C 44	36.6	14.0	618	12	CE048040		CE048040 tigr-gss-
C 45	36.6	14.0	672	11	BH514532		BH514532 BOHQL25TF

ALIGNMENTS

RESULT 1	CZ895441/c	CZ895441 upto001f0	Pine methylation unfiltered library (LibID: 131)
LOCUS			uppta001f002b10f0 Pine genomic, genomic survey sequence.
DEFINITION			Pinus taeda
ACCESSION	CZ895441	CZ895441	
VERSION	CZ895441.1	GI:75689927	
KEYWORDS	GSS		
SOURCE	Pinus taeda (loblolly pine)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.		
REFERENCE	1 (bases 1 to 563)		
AUTHORS	Rabinowicz, P.D., Citek, R.W., Budiman, M.A., Numberg, A., Bedell, J.A., Lakey, N., O'Shaughnessy, A.L., Nascimento, L.U., McCombie, W.R. and Martienssen, R.A.		
TITLE	Differential methylation of genes and repeats in land plants		
JOURNAL	Genome Res. 15 (10), 1431-1440 (2005)		
PUBMED	16204196		
COMMENT	Contact: Rabinowicz PD The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 795 7787 Fax: 301 838 0208 Email: pablo@tigr.org		
FEATURES	Location/Qualifiers 1. 563 /organism="Pinus taeda" /mol_type="genomic DNA" /db_xref="taxon:3352" /clone_lib="Pine methylation unfiltered library (LibID: 131)"		
Source			
ORIGIN			

563 GATAAGTTGAAAGTTGGCTTGCTGATTGTTGGCTGAACTGGTTTCCAAAGAGTTGTTAGGGTT 505

187 CATTTCAGGAAATAAGAAGGGCTTCGAACTGGTTTCCAAAGAGTTGTTAGGGTT 246

504 CATTTCAGGAAATAAGAAGGGCTTCGAACTGGTTTCCAAAGAGTTGTTAGGGTT 446

247 TTTCCACGGTCACCT 261

445 TTTTCAGGGTCACCT 431

RESULT 2

DR053876/c DR053876/c DR053876/c

LOCUS RTCA1_13_H01_g1_A029 RTCA1_13_H01_A029 5', mRNA sequence.

DEFINITION Roots minus calcium Pinus taeda cDNA clone

ACCESSION DR053876

VERSION DR053876.1 GI:66977443

EST. An EST database from calcium-deficient loblolly pine (Pinus taeda)

SOURCE Pinus taeda

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus. 1 to 674

COMMENT Contact: L., Cordonnier-Pratt, M.M., Lorenz, W.W., Zimmermann, C. and Dean, J.F.D.

TITLE An EST database from calcium-deficient loblolly pine (Pinus taeda)

roots

Unpublished (2005)

Other ESTs: RTCA1_13_H01.b1_A029

Contact: Cordonnier-Pratt, M.M.

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBR) and the CLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACCC).

Location/Qualifiers

1. 674 /organism="Pinus taeda"

/mol_type="mRNA"

/strain="3 CLONES"

/db_xref="taxon:3352"

/clone="RTCA1_13_H01_A029"

/lab_host="DH10B-T1"

/clone_lib="Roots minus calcium"

/note="Organ: Root; Vector: pSL1180; Site_1: EcorI; Site_2: XbaI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 139 days (July 28 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Starting five weeks prior to harvesting roots for mRNA preparation, the weekly fertilizer regimen for the potted trees was modified to omit calcium from the 0.5x Hoagland's solution (5 applications). For two days prior to starting the modified fertilizer regimen, pots were flushed extensively with water to reduce residual levels of calcium. Double-stranded cDNA was cloned

ORIGIN

Query Match 34.4%; Score 89.8; DB 9; Length 674;

Best Local Similarity 83.2%; Pred. NO. 3.9e-13;

Matches 114; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

EcORI (5' end) and XbaI (3' end)."

Qy 125 GAGATAAGTTGAAATAAGGCTTCGATTTGCTGAAATTTCTCTCACTATAAA 184

Db 511 GAGATAAGTTGAAATAAGGCTTCGATTTGCTGAAATTTCTCTCACTATAAA 453

Qy 185 AGCATTTCAGGAGCTTCGAACTGGTTTCCCAAGAGTTGTTAGGGGG 244

Db 452 GACATTTCAGAATAAGAAGCTCAACTGGTTTCCCAAGAGTTGTTAGGGGG 393

Qy 245 TTTTCCACGGTCACCT 261

Db 392 TATTCCAGGGTCACAT 376

RESULT 3

DR120385 DR120385

LOCUS RTMG1_29_H05_b1_A029 Roots minus magnesium Pinus taeda cDNA clone

DEFINITION RTMG1_29_H05_A029 3', mRNA sequence.

ACCESSION DR120385

VERSION DR120385.1 GI:67708695

KEYWORDS EST.

SOURCE Pinus taeda

ORGANISM Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus. 1 to 817

REFERENCE Pratt, L., Cordonnier-Pratt, M.M., Lorenz, W.W., Zimmermann, C. and Dean, J.F.D.

TITLE An EST database from magnesium-deficient loblolly pine (Pinus taeda) roots

JOURNAL Unpublished (2005)

COMMENT Contact: Cordonnier-Pratt, M.M.

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBR) and the CLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: M13-21 (TGTAAAACGACGGCCAGT).

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. 817 /organism="Pinus taeda"

/mol_type="mRNA"

/strain="3 CLONES"

/db_xref="taxon:3352"

/clone="RTMG1_29_H05_A029"

/lab_host="DH10B-T1"

/clone_lib="Roots minus magnesium"

/note="Organ: Root; Vector: pSL1180; Site_1: EcorI; Site_2: XbaI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 139 days (July 28 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Starting five weeks prior to harvesting roots for mRNA preparation, the weekly fertilizer regimen for the potted trees was modified to omit calcium from the 0.5x Hoagland's solution (5 applications). For two days prior to starting the modified fertilizer regimen, pots were flushed extensively with water to reduce residual levels of calcium. Double-stranded cDNA was cloned

source

Location/Qualifiers

1. 817 /organism="Pinus taeda"

/mol_type="mRNA"

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/clone="RTMG1_29_H05_A029"

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/clone_lib="Roots minus magnesium"

/note="Organ: Root; Vector: pSL1180; Site_1: EcorI; Site_2: XbaI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 139 days (July 28 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Starting five weeks prior to harvesting roots for mRNA preparation, the weekly fertilizer regimen for the potted trees was modified to omit calcium from the 0.5x Hoagland's solution (5 applications). For two days prior to starting the modified fertilizer regimen, pots were flushed extensively with water to reduce residual levels of calcium. Double-stranded cDNA was cloned

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:02:26 ; Search time 1779.21 Seconds
 (without alignments)
 9380.717 Million cell updates/sec

Title: US-09-973-994-131
 Perfect score: 261
 Sequence: 1 aggtgaccgtacagcattta.....gggtttttccacggtcacct 261

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : GenEmbl:*

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1: gb_env:*
2: gb_dat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_stb:*
8: gb_sy:*
9: gb_uni:*
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12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
C 1	42	16.1	171009	12	AC128851		AC128851 Rattus no
C 2	42	16.1	264832	12	AC106309		AC106309 Rattus no
C 3	41.8	16.0	38744	13	CEC56A3		Z77655 Caenorhabdi
C 4	41.2	15.8	161505	6	AC154234		AC154234 Mus muscu
C 5	41.2	15.8	222702	12	CT009561		CT009561 Mus muscu
C 6	40.8	15.6	1822957	12	CR931799		CR931799 Danio rer
C 7	40.8	15.6	259146	12	CT573231		CT573231 Danio rer
C 8	40.6	15.6	231271	12	AC117004		AC117004 Rattus no
C 9	40.6	15.6	232508	12	AC116189		AC116189 Rattus no
C 10	39.8	15.2	237705	12	AC171299		AC171299 Bos tauru
C 11	39.8	15.2	239162	12	AC175441		AC175441 Bos tauru
C 12	39.4	15.1	94646	12	AC171129		AC171129 Helobdell
C 13	39.2	15.0	158135	12	AC080040		AC080040 Homo sapi
C 14	39.2	15.0	174058	12	AC068695		AC068695 Homo sapi
C 15	39.2	15.0	176570	5	AC009499		AC009499 Homo sapi
C 16	38.8	14.9	33651	13	AC114261		AC114261 Dictyoste
C 17	38.8	14.9	195124	11	CR548625		CR548625 Zebratfish
C 18	38.8	14.9	208436	12	CT027756		CT027756 Danio rer

19	38.6	14.8	7942	10	HPV52
C 20	38.6	14.8	155399	5	PT027015
C 21	38.6	14.8	192290	12	AC153218
C 22	38.6	14.8	195220	12	AC151020
C 23	38.6	14.8	249791	11	BX537133
C 24	38.6	14.8	271777	12	AC157148
C 25	38.2	14.6	103409	11	AL662880
C 26	38.2	14.6	163804	11	BX05463
C 27	38.2	14.6	170688	6	AC101795
C 28	38.2	14.6	222137	12	CR954958
C 29	38.2	14.6	281676	12	AC171784
C 30	38	14.6	35850	13	AC006791
C 31	38	14.6	230810	12	AC118784
C 32	37.8	14.5	180309	5	AC073576
C 33	37.8	14.5	188107	5	CNS01DWE
C 34	37.8	14.5	264773	12	AC163148
C 35	37.6	14.4	73250	5	AC114946
C 36	37.6	14.4	114214	12	AP007470
C 37	37.6	14.4	168479	12	AC025384
C 38	37.6	14.4	224828	12	AC157113
C 39	37.4	14.3	40324	2	AX458634
C 40	37.4	14.3	110000	12	PFWML8P1_04
C 41	37.4	14.3	125632	4	AC015446
C 42	37.4	14.3	146130	12	AC015875
C 43	37.4	14.3	200195	5	AC146220
C 44	37.2	14.3	27426	5	AC079740
C 45	37.2	14.3	132822	12	AC181755
					Strongylo

ALIGNMENTS

RESULT 1	AC128851/c	171009 bp DNA linear HTG 20-NOV-2002
LOCUS	AC128851	Rattus norvegicus clone CH230-445E24, WORKING DRAFT SEQUENCE.
DEFINITION		
ACCESSION	AC128851	
VERSION	AC128851.3	GI:25139471
KEYWORDS		HTG; HTGS; PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE		Rattus norvegicus (Norway rat)
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE		1 (bases 1 to 171009)
AUTHORS		Muzny,D.Marie., Metzker,M., Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalabechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavarozzo,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chien,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Derman,C., Dernon,C., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escott,M., Eugenio,C., Evans,C.A., Falls,T., Fan,G., Ferrandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Geer,K., Gill,R., Grady,M., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodges,A., Hume,J., Hollins,B., Howells,S., Hulky,S., Hume,J., Idlebird,D., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelliy,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Louissegard,H., Lozano,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mallooy,K., Mangum,A., Mangum,B., Mapua,P., Martin,R., Martinez,E., McLeod,M.P., McLeod,M.P., McNeill,T.Z., Meenen,E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nnwaokeleme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valias, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

TITLE	JOURNAL	AUTHORS	COMMENT
Unpublished			
2 (bases 1 to 171009)			
Worley, K. C.			
Direct Submission			
Submitted (24-JUL-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
3 (bases 1 to 171009)			
Rat Genome Sequencing Consortium			
Direct Submission			
Submitted (20-NOV-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
On Nov 20, 2002 this sequence version replaced gi:23914598.			
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature			

Table.	Center: Genome Center
	Center: Baylor College of Medicine
	Center code: BCM
	Web site: http://www.hgsc.bcm.tmc.edu/
	Contact: hgsc-help@bcm.tmc.edu
	Project Information
	Center project name: KAVY
	Center clone name: CH230-445E24
	Summary Statistics
	Assembly program: Phrap; version 0.990329
	Consensus quality: 164467 bases at least Q40
	Consensus quality: 166274 bases at least Q30
	Consensus quality: 167295 bases at least Q20
	Estimated insert size: 171470; sum-of-contigs estimation
	Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
	NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
	NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
	This sequence will be replaced

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* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 171009: contig of 171009 bp in length.
  Location/Qualifiers
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  /organism="Rattus norvegicus"
  /mol_type="genomic DNA"
  /db_xref="taxon:10116"
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  clone_end:Sp6"
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  Best Local Similarity 47.7%; Pred. No. 0.019;
  Matches 123; Conservative 0; Mismatches 135; Indels 0; Q
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  Db 123083 TGGGGAGCAACCAAGAGCTCATGGTGTAGTATGTTACCGTTGGGAGTT
  Qy 64 CGAGATAAGTTGTAATTTGGCTGCTGATTGCTGAATATTCTCTCACTA
  Db 123023 TGCTCCTAACAAATGATAAAACTGAAAGAATATGTTAGCTTTAACCATTC
  Qy 124 CGAGATAAGTTGTAATTTGGCTGCTGATTGCTGAATATTCTCTCACTA
  Db 122963 TTTTACAAATTGATGTGTAAGATGACTTTACCTCCTAAATATATTGGACAT
  Qy 184 AAGCATTTCAGAAATAAGAAGGAGCTTCGAACTGGTTCCCAAGAGTTGTT
  Db 122903 GTCAATTATAATTATTAAAGAAATACAGATCTAGACTATTAAATTAGTTGTC
  Qy 244 GTTTTCCACGGTCACCT 261
  Db 122843 TTATTAAGCAAGGAGCTCCT 122826

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:21:26 ; Search time 125.935 Seconds
 (without alignments)
 4561.330 Million cell updates/sec

Title: US-09-973-994-79
 Perfect score: 307

Sequence: 1 gggtgcataccatggaaatggca.....gccccatcaactcgatcgacc 307

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_NA:
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:/*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:/*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:/*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:/*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:/*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:/*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:/*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:/*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:/*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfilesi.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	55.8	18.2	7218	2 US-09-232-463-14	Sequence 14, Appl	
2	36.4	11.9	63588	3 US-09-873-404-3	Sequence 3, Appl	
3	36.4	11.9	63588	3 US-10-243-735-3	Sequence 3, Appl	
4	36.4	11.9	63588	4 US-10-730-010-3	Sequence 3, Appl	
5	36.4	11.5	219964	3 US-09-949-016-15086	Sequence 15086, A	
6	35.4	11.2	101349	3 US-09-949-016-17433	Sequence 17433, A	
C	7	34.8	11.3	1664976	3 US-08-916-421B-1	Sequence 1, Appl
C	8	34.8	11.3	1664976	3 US-09-692-570-1	Sequence 1, Appl
C	9	34.6	11.3	5394	3 US-08-688-376-1	Sequence 1, Appl
C	10	34.4	11.2	764	3 US-09-949-016-5644	Sequence 5644, AP
C	11	34.4	11.2	764	3 US-09-949-016-5645	Sequence 5645, AP
C	12	34.4	11.2	1127	3 US-09-976-594-1102	Sequence 1102, AP
C	13	34	11.1	15756	3 US-09-949-016-13607	Sequence 13607, A
C	14	34	11.1	29165	3 US-09-949-016-12340	Sequence 12340, A
C	15	33.8	11.0	1141	3 US-09-806-708B-22	Sequence 22, Appl
C	16	33.4	10.9	453	3 US-09-328-352-2667	Sequence 2667, AP
C	17	33.4	10.9	601	3 US-09-949-016-64949	Sequence 64949, A
C	18	33.4	10.9	87863	3 US-09-949-016-14402	Sequence 14402, A
C	19	33.4	10.9	300402	3 US-09-949-016-13632	Sequence 13632, A
C	20	33	10.7	396	3 US-09-495-050A-98	Sequence 98, Appl
C	21	33	10.7	6854	2 US-08-468-036-4	Sequence 4, Appl
C	22	33	10.7	6854	2 US-08-376-843-4	Sequence 13528, A
C	23	33	10.7	24740	3 US-09-949-016-13528	Sequence 13528, A

ALIGNMENTS

RESULT 1	US-08-232-463-14	Sequence 14, Application US/08232463
		; Patent No. 5670367
		; GENERAL INFORMATION:
		; APPLICANT: DORNER, F.
		; APPLICANT: SCHEIFFLINGER, F.
		; APPLICANT: FALKNER, F. G.
		; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
		; NUMBER OF SEQUENCES: 52
		; CORRESPONDENCE ADDRESS:
		; ADDRESSEE: Foley & Lardner
		; STREET: 1800 Diagonal Road,
		; CITY: Alexandria
		; STATE: VA
		; COUNTRY: USA
		; ZIP: 22313-0299
		; COMPUTER READABLE FORM:
		; MEDIUM TYPE: Floppy disk
		; COMPUTER: IBM PC compatible
		; OPERATING SYSTEM: PC-DOS/MS-DOS
		; SOFTWARE: Patent In Release #1D, Version #1.25
		; CURRENT APPLICATION DATA:
		; APPLICATION NUMBER: US/08/232,463
		; FILING DATE:
		; CLASSIFICATION: 435
		; PRIOR APPLICATION DATA:
		; APPLICATION NUMBER: US/07/935,313
		; FILING DATE:
		; APPLICATION NUMBER: EP 91 114 300.6
		; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
		; FILING DATE: 26-AUG-1991
		; ATTORNEY/AGENT INFORMATION:
		; NAME: BENT, Stephen A.
		; REGISTRATION NUMBER: 29,768
		; TELECOMMUNICATION INFORMATION:
		; TELEPHONE: (703) 836-9300
		; TELEFAX: (703) 683-4109
		; TELEX: 899149
		; INFORMATION FOR SEQ ID NO: 14:
		; SEQUENCE CHARACTERISTICS:
		; LENGTH: 7218 base pairs
		; TYPE: nucleic acid
		; STRANDEDNESS: single
		; TOPOLOGY: linear
		; IMMEDIATE SOURCE:

CLONE: PTZgpt-F18
US-08-232-463-14

Query Match 18.2%; Score 55.8; DB 2; Length 7218;
Best Local Similarity 2.0%; Pred. No. 1.2e-06;
Matches 6; Conservative 186; Mismatches 103; Indels 0; Gaps 0;

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Db 1121 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1180

Qy 123 TCTTGCTCCCTAACATCCTATAAGGTCAATCTCATGCAAGAGATCTTGACAAATTGGAA 182
Db 1181 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1240

Qy 183 GAATCTGCCAATTGCTCCGCCCTCCTTAACCTGAAATTGGAAATCTGAACCC 242
Db 1241 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1300

Qy 243 TTCTGAGCTACCTGTTCTCTATCATGGCTTTCTTGCCATCACTC 297
Db 1301 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1355

RESULT 2
US-09-873-404-3
; Sequence 3, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(63588)
; OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

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Best Local Similarity 51.2%; Pred. No. 1.6;
Matches 85; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 106 CATTATTCTAGAATTCCTCTGGCTACCTGTTCTGAGCTTCACTGTTCT 271
Db 15012 CAGTCTTACTTGCACTGGCTTCTCCACCCCTCAGCAGCTTCACTGTTCT 271

Qy 166 TCTTGACAAATTGGAAAGAATCTGCTCCGCCCTCCTTAACAGTAGAAATTGGAT 15131
Db 15132 GGCTTCTTGGCTTCTCCACAGGAACTCCCTACAGGAACTGGGACTCC 15177

RESULT 3
US-10-243-735-3
; Sequence 3, Application US/10243735
; Patent No. 6706510

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:46:32 ; Search time 916.676 Seconds
 (without alignments)
 4115.199 Million cell updates/sec

Title: US-09-973-994-79
 Perfect score: 307
 Sequence: 1 ggtgcgatccatgttgcaccc 307

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Published Applications NA_Main:*

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13: /EMC_Celerra_SDSS3_ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SDSS3_ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SDSS3_ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SDSS3_ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	307	10	US-10-651-991-79
C 2	296	96.4	308	10	US-10-651-991-78
C 3	36.6	11.9	165156	10	US-10-995-561-13304
C 4	36.4	11.9	63588	6	US-10-243-735-3
C 5	36.4	11.9	63588	8	US-10-730-010-3
C 6	36	11.7	511	4	US-09-925-065A-261418
C 7	36	11.7	511	5	US-09-925-065A-261418
C 8	36	11.7	548	12	US-10-301-480-339709
C 9	36	11.7	548	12	US-10-301-480-953118
C 10	36	11.7	661	3	US-09-998-598-965
C 11	35.4	11.5	5976	8	US-10-437-963-8075
C 12	35.4	11.5	165156	8	US-10-741-601-56668
C 13	35.2	11.5	669	12	US-10-301-480-545653
C 14	35.2	11.5	669	12	US-10-301-480-1159062
C 15	35	11.4	445	3	US-09-920-300A-620
C 16	35	11.4	445	6	US-10-033-528-620
C 17	35	11.4	445	7	US-10-099-926-620

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18 35 11.4 445 10 US-10-961-527-620 Sequence 620, App
19 35 11.4 18820 3 US-09-764-891-6452 Sequence 6452, App
20 35 11.4 18820 6 US-10-205-428-733 Sequence 733, App
C 21 34.6 11.3 793 12 US-10-301-480-1174774 Sequence 1174774, Appl
C 22 34.6 11.3 3673778 7 US-10-312-841-1 Sequence 1, Appl
C 23 34.6 11.2 793 12 US-10-242-535A-21758 Sequence 21758, A
C 24 34.4 11.2 257 8 US-10-242-599-94708 Sequence 94708, A
C 25 34.4 11.2 306 8 US-10-242-535A-21758 Sequence 21758, A
C 26 34.4 11.2 321 8 US-10-242-535A-12694 Sequence 12694, A
C 27 34.4 11.2 321 8 US-10-242-535A-12694 Sequence 12694, A
C 28 34.4 11.2 426 8 US-10-242-535A-39856 Sequence 39856, A
C 29 34.4 11.2 426 8 US-10-242-535A-39856 Sequence 39856, A
C 30 34.4 11.2 436 8 US-10-242-535A-7614 Sequence 7614, App
C 31 34.4 11.2 436 8 US-10-242-535A-7614 Sequence 7614, App
C 32 34.4 11.2 436 8 US-10-242-535A-24125 Sequence 24125, A
C 33 34.4 11.2 482 8 US-10-242-535A-24125 Sequence 24125, A
C 34 34.4 11.2 533 8 US-10-242-535A-15691 Sequence 15691, A
C 35 34.4 11.2 533 8 US-10-242-535A-15691 Sequence 15691, A
C 36 34.4 11.2 533 8 US-10-242-535A-15691 Sequence 15691, A
C 37 34.4 11.2 540 16 US-10-128-061-3720 Sequence 3720, App
C 38 34.4 11.2 540 16 US-10-128-049-3720 Sequence 3720, App
C 39 34.4 11.2 541 4 US-09-925-065A-465048 Sequence 465048, A
C 40 34.4 11.2 541 4 US-09-925-065A-465049 Sequence 465049, A
C 41 34.4 11.2 541 5 US-09-925-065A-465048 Sequence 465048, A
C 42 34.4 11.2 541 5 US-09-925-065A-465049 Sequence 465049, A
C 43 34.4 11.2 544 12 US-10-301-480-521152 Sequence 521152, A
C 44 34.4 11.2 544 12 US-10-301-480-521153 Sequence 521153, A
C 45 34.4 11.2 544 12 US-10-301-480-1134561 Sequence 1134561, A

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ALIGNMENTS

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RESULT 1
US-10-651-991-79
Sequence 79, Application US/10651991
Publication No. US20050125161A1
GENERAL INFORMATION:
  APPLICANT: CAIRNEY, JOHN
  APPLICANT: XU, NANFIE
  TITLE OF INVENTION: DIFFERENTIALLY-EXPRESSED CONIFER CDNAs, AND THEIR USE
  TITLE OF INVENTION: IN IMPROVING SOMATIC EMBRYOGENESIS
  FILE REFERENCE: 7648.0023-00
  CURRENT APPLICATION NUMBER: US/10/651,991
  CURRENT FILING DATE: 2003-09-02
  PRIOR APPLICATION NUMBER: 60/239,250
  PRIOR FILING DATE: 2000-10-11
  PRIOR APPLICATION NUMBER: 60/260,882
  PRIOR FILING DATE: 2001-01-12
  NUMBER OF SEQ ID NOS: 339
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 79
  LENGTH: 307
  TYPE: DNA
  ORGANISM: Pinus taeda
US-10-651-991-79

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Query Match 100.0%; Score 307; DB 10; Length 307;
 Best Local Similarity 100.0%; Pred. No. 1.6e-81;
 Mismatches 0; Indels 0; Gaps 0;

Match 307; Conservative 0;

Qy 1 GTGGCGATCTAGAATTGCGATCTGGCTACTCCCTTGAATTAGAAGGCCTTC 60
 Db 1 GTGGCGATCTAGAATTGCGATCTGGCTACTCCCTTGAATTAGAAGGCCTTC 60

Qy 61 TTGCCACCTGGTCTTGAAGCATCTAGTCTTGAATTCTAGCTCATGCCAAGAGATCTTGAATTCTAGAAT 120
 Db 61 TTGCCACCTGGTCTTGAAGCATCTAGTCTTGAATTCTAGCTCATGCCAAGAGATCTTGAATTCTAGAAT 120

Qy 121 CCTCTTGGCTCTTAACATCCCTATAGGTCAATCTCATGCCAAGAGATCTTGAATTCTAGAAT 180
 Db 121 CCTCTTGGCTCTTAACATCCCTATAGGTCAATCTCATGCCAAGAGATCTTGAATTCTAGAAT 180

Qy 122 CCTCTTGGCTCTTAACATCCCTATAGGTCAATCTCATGCCAAGAGATCTTGAATTCTAGAAT 180
 Db 122 CCTCTTGGCTCTTAACATCCCTATAGGTCAATCTCATGCCAAGAGATCTTGAATTCTAGAAT 180

181	AAGAAATCTGCCAATTGCTCCGGCTCCTTAACCTCGAAAGTTGACTCTTAAGTTGCTGAA	240
181	AAGAAATCTGCCAATTGCTCCGGCTCCTTAACCTCGAAAGTTGACTCTTAAGTTGCTGAA	240
241	CCTTCTGAGCTTACCTGTTCTTGTCTATCATTGCTTTCTATCATTGCTTTCTATCATTGCTT	300
241	CCTTCTGAGCTTACCTGTTCTTGTCTATCATTGCTTTCTATCATTGCTTTCTATCATTGCTT	300
301	TCGGCACC 307	
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RESULT 2
6-10-651-991-78/c
Sequence 78, Application US/10651991
Publication No. US20050125161A1
GENERAL INFORMATION:
APPLICANT: CAIRNEY, JOHN
APPLICANT: XU, NANFIE
TITLE OF INVENTION: DIFFERENTIALLY-EXPRESSED CONIFER CDNAS, AND THEIR USE
TITLE OF INVENTION: IN IMPROVING SOMATIC EMBRYOGENESIS
FILE REFERENCE: 7648.0023-00
CURRENT APPLICATION NUMBER: US/10/651,991
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: 60/239,250
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/260,882
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 339
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 78

Query Match 96.4%; Score 296; DB 10; Length 308;
 Best Local Similarity 99.7%; Pred. No. 3.2e-78;
 Matches 307; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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308	GGTGGCATCCTAGAATTGCATCTGTTGCCGTTGCTAACCTCCCTTGAAATTAGAACCTTC	249
60	CTTGCCACCTGGTCTGAAGCATCCTTATTAGTCTTATTATCCTGGCATTATTCTTAGAA	119
248	CTTGCCACCTGGTCTGAAGCATCCTTATTAGTCTTATTATCCTGGCATTATTCTTAGAA	189
120	TCCTCTGCTCCCTAACATCCCTAACAGGTCACTCTCATGCCAAGAGATCTTGACAAATTG	179
188	TCCTCTGCTCCCTAACATCCCTAACAGGTCACTCTCATGCCAAGAGATCTTGACAAATTG	129
180	GAAGAATCTGCCAATTGCTCCGCCCTCCCTTAACCTCGAAAGTTGACTCTTAAGTTGCTGA	239
128	GAAGAATCTGCCAATTGCTCCGCCCTCCCTTAACCTCGAAAGTTGACTCTTAAGTTGCTGA	69
240	ACCTTCTGAGCTACCTGTTCTTGTCTTCTATCATTGCTTTCTTGTGCCATCACTCGG	299
68	ACCTTCTGAGCTACCTGTTCTTGTCTTCTATCATTGCTTTCTTGTGCCATCACTCGG	9
300	ATCGCACC 307	
8	ATCGCACC 1	

GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

RESULT 3
 3-10-995-561-13304/C
 Sequence 13304, Application US/10995561
 Publication No. US20050272054A1

1 // TITLE OF INVENTION : CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
1 // TITLE OF INVENTION : DETECTION AND USES THEREOF
1 // FILE REFERENCE: CL001559
1 // CURRENT APPLICATION NUMBER: US/10/995,561
1 // CURRENT FILING DATE: 2004-11-24
1 // NUMBER OF SEQ ID NOS: 85702
1 // SOFTWARE: FastSEQ for Windows Version 4.0
1 // SEQ ID NO 13304
1 // LENGTH: 165156
1 // TYPE: DNA
1 // ORGANISM: Homo sapiens

Query Match	11.9%	Score 36.6;	DB 10;	Length 165156;
Best Local Similarity	47.8%	Pred No. 32;		
Matches	119;	Conservative 5;	Mismatches 124;	Indels 1; Gaps 1;
	55	CCTTCCTTGCACCTGGTCTTGAAGCATCCTTATTAGTCTTATTATCCTTGGCATTATTCC	114	
	80842	CCTTCCTTCCTTCTTCTTGTAGGACCCCTTTGAGGACCTTCTYTCCTTCCCTCCCTCCC	80783	
Qy	115	TAGAATCCTCTGCTCCTTAACATCCTATAAGGTCAATCTCATGCCAAGAGATCTTGACAA	174	
Db	80782	TCCCTCCTCCCTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	80723	
Qy	175	ATTGGAAAGAAATCTGCCAATTGCTGCCCTCCCTTAACCTC-GAAGTTGACTCTCTAAAGT	233	
Db	80722	CTTCTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	80662	
Qy	234	TGCTGAACCTCTGAGCTACCTGTTCTGTTCTATGCTTCTATGCTTCTTGTGCCATC	293	
Db				
Qy	294	ACTCGGATC 302		
Db	80602	CACTGTATC 80594		
RESULT 4				
US-10-243-735-3				
; Sequence 3, Application US/10243735				
; Publication No. US20030022341A1				
; GENERAL INFORMATION:				
; APPLICANT: WEBSTER, Marion et al				
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC				
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES				
; TITLE OF INVENTION: THEREOF				
; FILE REFERENCE: CL001212DIV				
; CURRENT APPLICATION NUMBER: US/10/243,735				
; CURRENT FILING DATE: 2002-09-16				
; NUMBER OF SEQ ID NOS: 4				
; SOFTWARE: FastSEQ for Windows Version 4.0				
; SEQ ID NO 3				
; LENGTH: 63588				
; TYPE: DNA				
; ORGANISM: Human				
; FEATURE:				
; NAME/KEY: misc_feature				
; LOCATION: (1)..(63588)				
; OTHER INFORMATION: n = A,T,C or G				
US-10-243-735-3				
Query Match				
Best Local Similarity				
Matches 85; Conservative 0;				
Mismatches 81; Indels 0; Gaps 0;				
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Qy	166	TCTTGCACAAATTGGCAATCTGCCTTAACTCGAAGTGTGACT	225	
Db	15072	TCTCACCCAAATGCTGAGGGACTCCCAACTAGACTTCGCTCCTAACAGTAGAAATGGAT	15131	

Qy 79 GCATCCTTTAGTCATTATCCTGGCATTATCCTAGAATCCCTCTGCTCTTAACAT 138
 Db 4470 AAATACAATTAACCTTACCCATAACTATCTTAATTCGTTACTCTCATAT 4411

Qy 139 CCTATAAGGTCAATCTCATGCCAGAGATCTTGACAAATTGGAAATCTGCCAA 193
 Db 4410 AAATCAACACATAACTTTAACATACCTACTCTTACATTACAAACATAAA 4356

RESULT 2
 US-10-517-441-108/C
 Sequence 108, Application US/10517441

GENERAL INFORMATION:

APPLICANT: FOEKENS, John
 HARBECK, Nadia
 KOENIG, Thomas
 MAIER, Sabine
 MARTENS, John
 MODEL, Fabian
 NIMMRICH, Inko
 RUIJAN, Tamas
 SCHMITT, Armin
 SCHMITT, Manfred
 LOOK, Maxime P.
 MARX, Almuth
 HOEFLER, Heinz

TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
 TITLE OF INVENTION: Proliferative disorders

FILE REFERENCE: 47675-93

CURRENT APPLICATION NUMBER: US/10/517,441

PRIOR APPLICATION NUMBER: PCT/EP2003/010881

PRIOR FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: DE 10317955.0

PRIOR FILING DATE: 2003-04-17

PRIOR APPLICATION NUMBER: DE 10300096.8

PRIOR FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: DE 10245779.4

PRIOR FILING DATE: 2002-10-01

NUMBER OF SEQ ID NOS: 2147

SEQ ID NO: 108

LENGTH: 9353

TYPE: DNA

ORGANISM: Homo Sapiens

US-10-517-441-108

FILE REFERENCE: 2300-17767
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 CURRENT FILING DATE: 2004-07-08
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 PRIOR FILING DATE: 2002-01-08
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 SEQ ID NO: 222
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 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-501-187-222

Query Match 11.2%; Score 34.4; DB 6; Length 583;
 Best Local Similarity 59.0%; Pred. No. 0.66;
 Matches 59; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 68 CTGGTCCTGAAAGCATCCCTTAGCTTCTGCAATTCTAGAATCTCTCTTG 127
 Db 324 CAGGGTTTTGGCTTCTTGTGATATTTGGCAAGACGTTCTCCCTAGCTCTT 265

Qy 128 CTCCCTAACATCCTATAGGTCACTCATGCAAGAGATC 167
 Db 264 CTTCTTCACTTCCCTCATCATGATCCAAAGGGTC 225

RESULT 4
 US-11-266-748A-194452/C
 Sequence 194452, Application US/11266748A
 GENERAL INFORMATION:
 APPLICANT: Harkin, Paul
 APPLICANT: Johnston, Patrick
 APPLICANT: Mulligan, Karl
 TITLE OF INVENTION: Transcriptome Microarray Technology and
 Methods of Using the Same
 FILE REFERENCE: 55815-0102 (319189)
 CURRENT APPLICATION NUMBER: US/11/266,748A
 PRIOR APPLICATION NUMBER: EP 04105479.2
 CURRENT FILING DATE: 2005-11-03
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105479.2
 PRIOR FILING DATE: 2004-11-03
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 PRIOR APPLICATION NUMBER: EP 04105479.2
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105479.2
 PRIOR FILING DATE: 2004-11-03
 NUMBER OF SEQ ID NOS: 483996
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 194452
 LENGTH: 809
 TYPE: DNA
 ORGANISM: Homo Sapiens
 US-11-266-748A-194452

Query Match 11.2%; Score 34.4; DB 8; Length 809;
 Best Local Similarity 59.0%; Pred. No. 0.76;
 Matches 59; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 68 CTGGTCCTGAAAGCATCCCTTAGCTTCTGCAATTCTAGAATCTCTCTTG 127
 Db 490 CAGGGTTTTGGCTTCTTGTGATATTTGGCAAGACGTTCTCCCTAGCTCTT 431

Qy 128 CTCCCTAACATCCTATAGGTCACTCATGCAAGAGATC 167

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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:01:45 ; Search time 392.398 Seconds
 (without alignments)
 5454.872 Million cell updates/sec

Title: US-09-973-994-79
 Perfect score: 307
 Sequence: 1 gggtgcataccataatggca.....gccccatcactcgatcgacc 307

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_8:*

1: geneseqn1990s:*

2: geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	307	100.0	307	14	AEA49584		Aea49584 Loblolly
c	2	296	96.4	308	14	AEA49583	Aea49583 Loblolly
c	3	36.4	11.9	63588	8	AB557150	Abs557150 Human gen
c	4	36.2	11.8	2000	11	AC136306	Ac136306 Rice stre
c	5	36	11.7	661	6	ABV87654	Abv87654 Human col
c	6	35.8	11.7	677	1	AAN60393	Aan60393 Sequence
c	7	35.8	11.7	9353	13	ADS89445	Ads89445 Oligonucl
c	8	35.6	11.6	265118	5	AAH41227	Aah41227 Pyrococcus
c	9	35.4	11.5	165156	13	ADS36459	Ads36459 Human aut
c	10	35	11.4	445	6	ABK45069	Abk45069 cDNA enco
c	11	35	11.4	2607	14	ADW16473	Adw16473 Eucalyptu
c	12	35	11.4	9353	13	ADS89092	Ads89092 Human AKR
c	13	35	11.4	18820	4	AAL03764	Aal03764 Human rep
c	14	35	11.4	18820	4	ABA07938	Aba07938 Human ova
c	15	34.8	11.3	64976	2	AAV21209_16	Continuation (17 O
c	16	34.6	11.3	5394	2	AAUT00872	Aat00872 Murine mC
c	17	34.6	11.3	5394	3	AAZ86916	Aaz86916 Mouse mC2
c	18	34.6	11.3	5394	14	AEC05449	Aec05449 Mouse mC2

ACN37817 Tumour-as

Acn37818 Insulin-s

Adz48889 Human

Adz48890 Human

Aak53287 Human

Aed73250 Human

Adx54786 Plant ful

Continuation (4 of

Ads89719 Oligonucl

Aaf16377 Human pro

Abq60765 Human col

Adl13373 Human

Aad08441 Human

Aad05439 Human

Aas85654 DNA

Aed73250 Human

Adz70690 Human

Adz48891 Human

Adz165341 Human

Aee10567 Hamster

Adk11816 Breast

Ac153983 Human

Abk44654 cDNA

Abk45341 cDNA

Aee14209 Hamster

Aee14209 Hamster

Abv89065 Human

CC for use in breeding trees with superior characteristics for use in
 CC production of paper and other wood products.

XX Sequence 307 BP; 62 A; 84 C; 51 G; 110 T; 0 U; 0 Other;

SQ Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 100.0%; Score 307; DB 14; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.2e-79;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC plant clones, determining embryo fitness, and selecting advantageous
 CC conditions for embryo development. The invention is particularly intended
 CC for use in breeding trees with superior characteristics for use in
 CC production of paper and other wood products.

XX SQ Sequence 308 BP; 110 A; 51 C; 84 G; 63 T; 0 U; 0 Other;
 XX Best Local Similarity 99.7%; Pred. No. 2e-76;
 XX Matches 307; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 XX Query Match 96.4%; Score 296; DB 14; Length 308;
 XX Best Local Similarity 99.7%; Pred. No. 2e-76;
 XX Matches 307; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 XX Query Match 1 GGTGGATCTAGAATTGCAATCTGGCATCTGGTGGCTTGCCTTC 59
 XX DB 308 GGTGGATCTAGAATTGCAACTCCCTTGAATTAGAACGGCTTC 249
 XX Query Match 60 CTTGCCACCTGGCTTGAAGCATCTTGTGGCATTATCCTTGC 119
 XX DB 248 CCTCTTGTGCTCCTAAACATCCTAAGGTCACTCATGCCAAGAGATCTTGC 189
 XX Query Match 120 CCTCTTGTGCTCCTAAACATCCTAAGGTCACTCATGCCAAGAGATCTTGC 179
 XX DB 188 CCTCTTGTGCTCCTAAACATCCTAAGGTCACTCATGCCAAGAGATCTTGC 129
 XX Query Match 180 GAAGAATCTGCCAATTGCTCCCTCCCTTAACCTGAAGTTGACTCTCA 239
 XX DB 128 GAAGAATCTGCCAATTGCTCCCTCCCTTAACCTGAAGTTGACTCTCA 69
 XX Query Match 240 ACCTTCTGAGCTACCTGTTCTTGTGCTTCTTGTGCCATCACTCG 300
 XX DB 68 ACCTTCTGAGCTACCTGTTCTTGTGCTTCTTGTGCCATCACTCG 9
 XX Query Match 300 ATCGCACC 307
 XX DB 8 ATCGCACC 1
 XX
 RESULT 2
 AEA49583/C
 ID AEA49583 standard; cDNA; 308 BP.
 XX AC AEA49583;
 XX DT 11-AUG-2005 (first entry)
 XX DE Loblolly pine cDNA clone, LPS-095, SEQ ID 78.
 XX KW Plant; embryogenesis; plant breeding; paper; wood; ss.
 XX OS Pinus taeda.
 XX PN US2005125161-A1.
 XX PD 09-JUN-2005.
 XX PF 02-SEP-2003; 2003US-00651991.
 XX PR 11-OCT-2000; 2000US-0239250P.
 XX PR 12-JAN-2001; 2001US-0260882P.
 XX PR 11-OCT-2001; 2001US-00973994.
 XX PA (PAPE-) INST PAPER SCI & TECHNOLOGY INC.
 XX Cairney J, Xu N;
 XX DR WPI; 2005-417092/42.
 XX PT Relational database of cDNA molecules including those corresponding to
 PT Loblolly pine major intrinsic protein, being differentially expressed
 PT during plant embryogenesis, useful for staging plant embryos.
 XX PS Claim 17; SEQ ID NO 78; 219pp; English.
 XX CC The present invention relates to a relational database of cDNA molecules
 CC comprising multiple nucleotide sequences (AEA49506-AEA49832). The
 CC database is useful for staging plant embryos, selecting advantageous.

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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 07:10:56 ; Search time 3077.57 Seconds
(without alignments)
5578.184 Million cell updates/sec

Title: US-09-973-994-79
Perfect score: 307
Sequence: 1 gggcgatccataatggca.....gccccatcactggatcgacc 307

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
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 library (Male) produced by Pieter de Jong"

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Db 111 TTCTAGAATTCCTCCTAACATCTAACATCTAACATGCTCATGCCAAGAGATCTTG 170
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Qy 171 ACAAAATTGGAAAGAACATTGCCAACATTGCTCCTAACACTGAAACTTGACTCTCA 230
 139 ATGATCTCACTTATATGTGGAATTGGAAATTGCTCAACTTTAAATACTCAATCTTATGTTGTA 198

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RESULT 3
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LOCUS AL794888 466 bp mRNA linear EST 13-NOV-2003
 DEFINITION AL794888 XGC-neurula Xenopus tropicalis cDNA clone TNeu115b01 5',
 mRNA sequence.

ACCESSION AL794888
 VERSION AL794888.2 GI:38316656
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 466)
 AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 TITLE Sanger Xenopus EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Jun 25, 2002 this sequence version replaced gi:21580592.
 Contact: Taylor R
 Sanger Institute
 Hinxtion, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn. This sequence was from a Xenopus
 cDNA was oligo dT primed from Sug of poly A+ RNA from neurula.
 EcoRI-NotI cut cDNA was then ligated into PCS107 with EcoRI at the
 5' end and NotI at the 3' end.

Vector: PCS107; Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli DH10B
 Sanger Xenopus tropicalis EST project 2001
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 Sequencing primer: SP6
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RESULT 2
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LOCUS 997 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TBT3 end of BAC #
 BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL060767
 VERSION 1 GI:4943573
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydrioidea; Drosophilidae; Drosophila.
 1 (bases 1 to 997)
 Genoscope.

Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequecage :
 BP 1911 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library,
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES Location/Qualifiers
 Source

COMMENT

1. .997 /organism="Drosophila melanogaster"
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GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucléic - nucleic search, using sw model

Run on: July 11, 2006, 07:02:26 ; Search time 2092.79 Seconds
 (without alignments)
 9380.717 Million cell updates/sec

Title: US-09-973-994-79
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*

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15: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

Summaries

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1	55.8	18.2	7218	2 I66494	I66494 Sequence 14
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3	42	13.7	110000	12 AC121678_4	Continuation (5 of
4	40.4	13.2	230071	12 AC132699	AC132699 Rattus no
C	50.4	13.2	338915	12 AC130523	AC130523 Rattus no
C	39.8	13.0	45027	13 CBRG39N14	AC084575 Caenorhab
7	39	12.7	224084	12 CR318629	CR318629 Danio rer
8	39	12.7	237446	11 BX546500	BX546500 Zebrafish
9	38.8	12.6	110000	12 AC107427_1	Continuation (2 of
10	38.6	12.6	7761	10 OPU83594_	U83594 Ovine papil
11	38.4	12.5	171562	5 AC107027	AC107027 Homo sapi
C	38.4	12.5	197206	12 AC023757	AC023757 Homo sapi
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C	38.4	12.5	234072	12 AC099135	AC099135 Rattus no
C	38.2	12.4	183481	12 AC120912	AC120912 Rattus no
16	38.2	12.4	234844	12 AC111734	AC111734 Rattus no
C	38	12.4	187571	12 AC177302	AC177302 Strongylo
C	38	12.4	221478	12 AC079545	AC079545 Mus muscu

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.8	18.2	7218	2 I66494	I66494 Sequence 14
2	42.6	13.9	230556	12 AC162231	AC162231 Bos tauru
3	42	13.7	110000	12 AC121678_4	Continuation (5 of
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8	39	12.7	237446	11 BX546500	BX546500 Zebrafish
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16	38.2	12.4	234844	12 AC111734	AC111734 Rattus no
C	38	12.4	187571	12 AC177302	AC177302 Strongylo
C	38	12.4	221478	12 AC079545	AC079545 Mus muscu

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c 24 37.6 12.2 184463 6 AC126553
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c 31 37.4 12.2 237286 12 AC113645
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c 35 37 12.1 52052 12 AC100081
c 36 37 12.1 123748 6 BX678774
c 37 37 12.1 177857 12 AC135432
c 38 37 12.1 202838 12 CR38230
c 39 36.8 12.0 85903 12 AC177439
c 40 36.8 12.0 120077 4 AC148292
c 41 36.8 12.0 137281 12 AC124217
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c 43 36.8 12.0 217726 6 AL928680
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ALIGNMENTS

RESULT 1
I66494 LOCUS I66494
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1
KEYWORDS GI:2724471
SOURCE Unknown
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 7218)
  Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
  Recombinant Fowlpox virus
  Patent: US 5670367-A 14-23-1997
  JOURNAL
  FEATURES
  1. 7218
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